

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/539,110
Source: IFWP
Date Processed by STIC: 2/26/07

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/539,110

DATE: 02/26/2007
TIME: 12:03:45

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02262007\J539110.raw

3 <110> APPLICANT: HALOZYME INC.
4 Frost, Gregory I.
5 Kundu, Anirban
6 Bookbinder, Louis H.
8 <120> TITLE OF INVENTION: HUMAN CHONDROITINASE GLYCOPROTEIN (CHASEGP), PROCESS FOR
PREPARING THE
9 SAME, AND PHARMACEUTICAL COMPOSITIONS COMPRISING THEREOF
11 <130> FILE REFERENCE: HALO1330-1 (Formerly DELIA1330-1)
13 <140> CURRENT APPLICATION NUMBER: US 10/539,110
C--> 14 <141> CURRENT FILING DATE: 2005-06-13
16 <150> PRIOR APPLICATION NUMBER: PCT/US 03/40090
17 <151> PRIOR FILING DATE: 2003-12-15
19 <150> PRIOR APPLICATION NUMBER: US 60/433,532
20 <151> PRIOR FILING DATE: 2002-12-16
22 <160> NUMBER OF SEQ ID NOS: 10
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 481
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <400> SEQUENCE: 1
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37 Val His Leu Thr Ser Trp Leu Leu Ile Phe Phe Ile Leu Lys Ser Ile
38 20 25 30
41 Ser Cys Leu Lys Pro Ala Arg Leu Pro Ile Tyr Gln Arg Lys Pro Phe
42 35 40 45
45 Ile Ala Ala Trp Asn Ala Pro Thr Asp Gln Cys Leu Ile Lys Tyr Asn
46 50 55 60
49 Leu Arg Leu Asn Leu Lys Met Phe Pro Val Ile Gly Ser Pro Leu Ala
50 65 70 75 80
53 Lys Ala Arg Gly Gln Asn Val Thr Ile Phe Tyr Val Asn Arg Leu Gly
54 85 90 95
57 Tyr Tyr Pro Trp Tyr Thr Ser Gln Gly Val Pro Ile Asn Gly Gly Leu
58 100 105 110
61 Pro Gln Asn Ile Ser Leu Gln Val His Leu Glu Lys Ala Asp Gln Asp
62 115 120 125
65 Ile Asn Tyr Tyr Ile Pro Ala Glu Asp Phe Ser Gly Leu Ala Val Ile
66 130 135 140
69 Asp Trp Glu Tyr Trp Arg Pro Gln Trp Ala Arg Asn Trp Asn Ser Lys
70 145 150 155 160
73 Asp Val Tyr Arg Gln Lys Ser Arg Lys Leu Ile Ser Asp Met Gly Lys
74 165 170 175
77 Asn Val Ser Ala Thr Asp Ile Glu Tyr Leu Ala Lys Val Thr Phe Glu

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82	195	200	205
85	Ser Arg Pro Lys Gly Leu Trp	Gly Tyr Tyr Leu Tyr	Pro Asp Cys His
86	210	215	220
89	Asn Tyr Asn Val Tyr Ala Pro Asn	Tyr Ser Gly Ser	Cys Pro Glu Asp
90	225	230	235
93	Glu Val Leu Arg Asn Asn Glu	Leu Ser Trp	Leu Trp Asn Ser Ser Ala
94	245	250	255
97	Ala Leu Tyr Pro Ser Ile Cys Val	Trp Lys Ser	Leu Gly Asp Ser Glu
98	260	265	270
101	Asn Ile Leu Arg Phe Ser Lys	Phe Arg Val His	Glu Ser Met Arg Ile
102	275	280	285
105	Ser Thr Met Thr Ser His Asp	Tyr Ala Leu Pro	Val Phe Val Tyr Thr
106	290	295	300
109	Arg Leu Gly Tyr Arg Asp	Glu Pro Leu Phe	Phe Leu Ser Lys Gln Asp
110	305	310	315
113	Leu Val Ser Thr Ile Gly Glu	Ser Ala Ala	Leu Gly Ala Ala Gly Ile
114	325	330	335
117	Val Ile Trp Gly Asp Met Asn	Leu Thr Ala Ser	Lys Ala Asn Cys Thr
118	340	345	350
121	Lys Val Lys Gln Phe Val	Ser Ser Asp	Leu Gly Ser Tyr Ile Ala Asn
122	355	360	365
125	Val Thr Arg Ala Ala Glu Val	Cys Ser	Leu His Leu Cys Arg Asn Asn
126	370	375	380
129	Gly Arg Cys Ile Arg Lys	Met Trp Asn Ala Pro	Ser Tyr Leu His Leu
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133	Asn Pro Ala Ser Tyr His	Ile Glu Ala Ser	Glu Asp Gly Glu Phe Thr
134	405	410	415
137	Val Lys Gly Lys Ala Ser Asp	Thr Asp	Leu Ala Val Met Ala Asp Thr
138	420	425	430
141	Phe Ser Cys His Cys Tyr Gln	Gly Tyr Glu	Gly Ala Asp Cys Arg Glu
142	435	440	445
145	Ile Lys Thr Ala Asp Gly Cys	Ser Gly Val Ser	Pro Ser Pro Gly Ser
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153	Leu		480
157	<210> SEQ ID NO: 2		
158	<211> LENGTH: 481		
159	<212> TYPE: PRT		
160	<213> ORGANISM: Mus musculus		
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181	50	55	60	
184	Leu Thr Leu Asn Leu Lys Val Phe Gln Met Val Gly Ser Pro Arg Leu			
185	65	70	75	80
188	Lys Asp Arg Gly Gln Asn Val Val Ile Phe Tyr Ala Asn Arg Leu Gly			
189	85	90	95	
192	Tyr Tyr Pro Trp Tyr Thr Ser Glu Gly Val Pro Ile Asn Gly Gly Leu			
193	100	105	110	
196	Pro Gln Asn Thr Ser Leu Gln Val His Leu Lys Gly Ala Gly Gln Asp			
197	115	120	125	
200	Ile Asn Tyr Tyr Ile Pro Ser Glu Asn Phe Ser Gly Leu Ala Val Ile			
201	130	135	140	
204	Asp Trp Glu Tyr Trp Arg Pro Gln Trp Ala Arg Asn Trp Asn Thr Lys			
205	145	150	155	160
208	Asp Ile Tyr Arg Gln Lys Ser Arg Thr Leu Ile Ser Asp Met Lys Glu			
209	165	170	175	
212	Asn Ile Ser Ala Ala Asp Ile Glu Tyr Ser Ala Lys Ala Thr Phe Glu			
213	180	185	190	
216	Lys Ser Ala Lys Ala Phe Met Glu Glu Thr Ile Lys Leu Gly Ser Lys			
217	195	200	205	
220	Ser Arg Pro Lys Gly Leu Trp Gly Tyr Tyr Leu Tyr Pro Asp Cys His			
221	210	215	220	
224	Asn Tyr Asn Val Tyr Ala Thr Asn Tyr Thr Gly Ser Cys Pro Glu Glu			
225	225	230	235	240
228	Glu Val Leu Arg Asn Asn Asp Leu Ser Trp Leu Trp Asn Ser Ser Thr			
229	245	250	255	
232	Ala Leu Tyr Pro Ala Val Ser Ile Arg Lys Ser Phe Ala Asp Ser Glu			
233	260	265	270	
236	Asn Thr Leu His Phe Ser Arg Phe Arg Val Arg Glu Ser Leu Arg Ile			
237	275	280	285	
240	Ser Thr Met Thr Ser Gln Asp Tyr Ala Leu Pro Val Phe Val Tyr Thr			
241	290	295	300	
244	Gln Leu Gly Tyr Lys Glu Glu Pro Leu Leu Phe Pro Phe Lys Gln Asp			
245	305	310	315	320
248	Leu Ile Ser Thr Ile Gly Glu Ser Ala Ala Leu Gly Ala Ala Gly Ile			
249	325	330	335	
252	Val Val Trp Gly Asp Met Asn Leu Thr Ser Ser Glu Glu Asn Cys Thr			
253	340	345	350	
256	Lys Val Asn Arg Phe Val Asn Ser Asp Phe Gly Ser Tyr Ile Ile Asn			
257	355	360	365	
260	Val Thr Arg Ala Ala Glu Val Ser Ser Arg His Leu Cys Lys Asn Asn			
261	370	375	380	
264	Gly Arg Cys Val Arg Lys Thr Trp Lys Ala Ala His Tyr Leu His Leu			
265	385	390	395	400
268	Asn Pro Ala Ser Tyr His Ile Glu Ala Ser Glu Asp Gly Glu Phe Ile			
269	405	410	415	

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272 Val Arg Gly Arg Ala Ser Asp Thr Asp Leu Ala Val Met Ala Glu Asn
 273 420 425 430
 276 Phe Leu Cys His Cys Tyr Glu Gly Tyr Glu Gly Ala Asp Cys Arg Glu
 277 435 440 445
 280 Met Thr Glu Ala Ser Gly Pro Ser Gly Leu Ser Leu Ser Ser Ser
 281 450 455 460
 284 Val Ile Thr Leu Cys Leu Leu Val Leu Ala Gly Tyr Gln Ser Ile Gln
 285 465 470 475 480
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292 <210> SEQ ID NO: 3

293 <211> LENGTH: 2414

294 <212> TYPE: DNA

295 <213> ORGANISM: Homo sapiens

297 <400> SEQUENCE: 3

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302	cgcgtcagcc	actgcctcct	gggttcagggt	gattctcctg	acttagcctc	ctgagtggct	180
304	gggactgcag	gagcatgccca	tcatgcccag	ctgattttt	tattttttagt	agagatgggg	240
306	tttcaccgtg	ttggccagaa	tggtttgcat	tcctgacctc	aagtgtatcg	cctgcctcag	300
308	cctcccaaaa	tgttgggtac	aggggtgagc	caccgtgcct	tgctattaat	gccatctatt	360
310	tcactgaaga	ttccgcctct	catttcttga	gtcattttt	ttaaatttcc	ttaaatttggaa	420
312	cttcacattt	tctgatgcct	ccttggttag	cttaataact	gaccttctga	attttttttt	480
314	aggaaaatca	ggaatttctt	cttgggttgg	agccattgt	ggacatcctt	tgccattcaa	540
316	cctctgattt	gcacaagggt	actaaaggac	cagcagcaaa	caaaacgttt	ggtcttctag	600
318	agtgcactaa	agcagaagat	acgtaacatt	tttacatc	catgaaagta	ttatctgaag	660
320	gacagttaaa	gctttgtgtt	gttcaaccag	tacatctac	ttcatggctc	tttatatttt	720
322	ttattctaaa	gtctatctct	tgtctaaaac	ctgctcgact	tccaatttt	caaaggaaac	780
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326	taaatttga	aatgttccct	gtgattggaa	gcccactggc	caaggccagg	ggccaaaatg	900
328	tcactatatt	ttatgtcaac	agattgggat	actatccgtg	gtatacatca	cagggggtcc	960
330	ccattaatgg	aggctccca	cagaacataa	gtttacaagt	acatctggaa	aaagctgacc	1020
332	aagatattaa	ttattacatc	cctgctgaag	atttcagtgg	acttgctgtt	atagatttggg	1080
334	aatatttggag	accacagtgg	gcccggaaact	ggaactcaa	agatgttac	agacagaagt	1140
336	caagaaagct	tatttccgat	atgggaaaga	atgtatcagc	taccgatatt	gaatattttag	1200
338	ccaaagtgac	ctttgaagaa	agtgc当地	ctttcatgaa	ggaaaccatc	aaatttggaa	1260
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348	ggatctccac	catgacatct	catgattatg	ctctgcctgt	atttgc	acaaggctag	1560
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352	aaagtgc	cttggggact	gcaggcattt	ttatttgggg	agacatgaat	ttaactgc	1680
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358	gcataaggaa	gatgtggaaac	gcccggcagg	accttcactt	gaaccctgca	agttaccaca	1860
360	tagggcctc	tgaggacggg	gagtttactg	tgaaaggaaa	agcatctgat	acagacctgg	1920
362	cagtgc	atgatcattt	tcctgtcatt	gttac	cagg	atatgaagga	1980
364	gagaaataaa	gacggctgat	ggctgc	gggttcccc	ttctcctggt	tcactaatga	2040
366	cacttgc	actgttttta	gcaagttatc	gaagcattca	gttgc	gagat	2100

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368	aaagggaatt	gtgtggcctc	tagcctagtc	atttaaagaa	ggatgttaact	tataacattt	2160
370	tttttctctt	atgaattcta	ttgagagata	ttataagttag	acattatgt	tgtcacttaa	2220
372	cataaacaga	aacattattt	tattgcctc	cagtcggct	aggaaaccag	atctgggta	2280
374	aagtcaatgt	acacttcctc	cttattggaa	tatttaagtt	gcatttaaac	taaaactagt	2340
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391	tgtggcaaaac	ctgtctccac	ccaaggaaata	gctattcacc	ttttcgta	actggaaagag	180
393	tgaaccaaag	aggcctttt	gattacgtt	aagaaaaggt	agtgaaggtt	ctatcttac	240
395	atgcaactat	tgcctgaagg	acaattaaga	ctctgtgtt	ttcaaccagt	acatcttaca	300
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